

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run On: April 28, 2003, 13:49:30 ; Search time 26 Seconds
(without alignments)
3412.772 Million cell updates/sec

Title: US-09-497-822C-19
Perfect score: 4912
Sequence: 1 MEVQLGLGRVYRPPSKTYR.....SVQVPKILSGKVRPIVFHQ 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4880	99.3	919	2 A39248	androgen receptor
2	4798.5	97.7	910	2 A34721	androgen receptor
3	4763	97.0	911	2 B34721	androgen receptor
4	4206.5	85.6	902	2 B40494	androgen receptor
5	4176	85.0	899	2 A35895	androgen receptor
6	1676	34.1	344	2 I51330	androgen receptor
7	1523	31.0	848	2 JG0194	androgen receptor
8	1262.5	25.7	930	2 A25923	androgen receptor
9	1262	25.7	933	1 ORHUP	progesterone recep
10	1234	25.1	923	2 I53280	progesterone recep
11	1218	24.8	786	2 A35466	progesterone recep
12	1205	24.5	923	2 A39596	progesterone recep
13	1092	22.2	981	2 A41401	progesterone recep
14	1078.5	22.0	984	2 A29513	mineralocorticoid
15	1065	21.7	795	1 ORRTG	mineralocorticoid
16	1063.5	21.7	783	1 A25691	glucocorticoid rec
17	1054.5	21.5	776	1 S44047	glucocorticoid rec
18	1042	21.2	777	1 ORHUGA	glucocorticoid rec
19	1023	20.8	758	2 S60586	glucocorticoid rec
20	1003	20.4	771	2 A54273	glucocorticoid rec
21	943.5	19.2	742	1 ORHUGB	glucocorticoid rec
22	715	14.6	166	2 S35795	glucocorticoid rec
23	502	10.2	595	2 I47140	androgen receptor
24	491	10.0	586	1 QRXLE	estradiol receptor
25	485.5	9.9	600	1 QRRE	estrogen receptor
26	478	9.7	595	1 QRHTE	estrogen receptor
27	478	9.7	701	2 S64737	estrogen receptor
28	474	9.6	589	1 ORCHE	estrogen receptor
29	474	9.6	599	1 QRNSE	estrogen receptor

30	461.5	9.4	620	2 T10423	estrogen receptor
31	448	9.1	535	2 S58224	estrogen receptor
32	444	9.0	574	2 A37197	estrogen receptor
33	442	9.0	503	2 JWO046	estrogen receptor
34	437.5	8.9	477	2 S71400	estrogen receptor
35	437.5	8.9	530	2 JC5939	estrogen receptor
36	398.5	8.1	1043	2 T13733	estrogen receptor
37	391	8.0	433	2 S58087	estrogen receptor
38	387.5	7.9	433	2 B29345	estrogen receptor
39	383	7.8	521	2 A29345	estrogen receptor
40	379	7.7	462	2 S44490	estrogen receptor
41	370.5	7.5	543	2 A32693	estrogen receptor
42	364.5	7.4	746	2 B32693	estrogen receptor
43	357	7.3	533	2 S37781	estrogen receptor
44	346	7.0	422	2 I48305	estrogen receptor
45	343.5	7.0	423	2 S02710	estrogen receptor

ALIGNMENTS

RESULT 1
A39248
androgen receptor - human
C:Species: Homo sapiens (man)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C:Accession: A39248; A30328; A40109; A60946; A34942; A27653; A40108; A40494; A32224;
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
A>Title: Sequence of the intron/exon junctions of the coding region of the human andr
A:Reference number: A39248; MUID:90083302; PMID:2594783
A:Accession: A39248
A:Molecule type: DNA
A:Residues: 1-919 <LUB>
A:Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906
R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkma
Mol. Cell. Endocrinol. 61, 257-262, 1989
A>Title: The N-terminal domain of the human androgen receptor is encoded by one, larg
A:Reference number: A30328; MUID:89137730; PMID:2917688
A:Accession: A30328
A:Molecule type: DNA
A:Residues: 1-777-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>
A:Cross-references: GB:M20260
R:Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson, E.
Science 240, 327-330, 1988
A>Title: Cloning of human androgen receptor complementary DNA and localization to the
A:Reference number: A40109; MUID:88178112; PMID:3353727
A:Accession: A40109
A:Molecule type: DNA
A:Residues: 559-624 <LU2>
A:Cross-references: GB:M20132
R:Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Ris-Sta
J. Mol. Endocrinol. 2, R1-R4, 1989
A>Title: Structural organization of the human androgen receptor gene.
A:Reference number: A60946; MUID:89322749; PMID:2546571
A:Accession: A60946
A:Molecule type: DNA
A:Residues: 536-540; 587-591; 626-631; 723-726; 770-774; 814-818; 867-870 <KUI>
R:Lubahn, D.B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, F.
Mol. Endocrinol. 2, 1265-1275, 1988
A>Title: The human androgen receptor: complementary deoxyribonucleic acid cloning, se
A:Reference number: A34942; MUID:89112208; PMID:3216866
A:Accession: A34942
A:Molecule type: mRNA
A:Residues: 1-919 <LU3>
A:Cross-references: GB:M20132; NID:g178627; PIDN:AAA51729.1; PID:g178628; GB:J03180
R:Trapani, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;
Biochem. Biophys. Res. Commun. 153, 241-248, 1988
A>Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
A:Reference number: A27653; MUID:88240407; PMID:3377788
A:Accession: A27653
A:Molecule type: mRNA
A:Residues: 468-564, 'K', 566-919 <TRA>

Fri May 9 14:20:43 2003

A:Cross-references: GB:M20260; NID:g178891; PIDN:AAA51774.1; PID:g178892
A:Note: the authors translated the codon AAG for residue 565 as Glu
R:Chang, C.; Kokontis, J.; Liao, S.
Science 240, 324-326, 1988
A:Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor
A:Reference number: A40108; MUID:88178111; PMID:3353726
A:Accession: A40108
A:Molecule type: mRNA
A:Residues: 557-628 <CHA>
A:Cross-references: GB:M18624
R:Chang, C.; Kokontis, J.; Liao, S.
Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
A:Title: Structural analysis of complementary DNA and amino acid sequences of human and
A:Reference number: A40494; MUID:89017168; PMID:3174628
A:Accession: A40494
A:Molecule type: mRNA
A:Residues: 1-74, 79-89, 'H', 90-472, 'GGG', 473-474, 'E', 476-644, 'N', 646-919 <CH2>
A:Cross-references: GB:M23263
R:Tilley, W.D.; Marcelli, M.; Wilson, J.D.; McPhaul, M.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 327-331, 1989
A:Title: Characterization and expression of a cDNA encoding the human androgen receptor
A:Reference number: A32224; MUID:89098909; PMID:2911578
A:Accession: A32224
A:Molecule type: mRNA
A:Residues: 1-77, 79-211, 'R', 213-471, 473-919 <TIL>
A:Cross-references: GB:M21748; GB:J04150; NID:g178871; PIDN:AAA51771.1; PID:g178872
R:Nowosowicz, I.; Lee, H.J.; Chen, H.T.; Mestayer, C.; Portois, M.C.; Cabrol, S.; Mauval
Mol. Endocrinol. 7, 861-869, 1993
A:Title: A point mutation in the second zinc finger of the DNA-binding domain of the and
A:Reference number: A40715; MUID:94019395; PMID:8413310
A:Accession: A40715
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 557-614, 'H', 616-624 <MOM>
A:Cross-references: PIDN:AAB28340.1; PID:g425580
C:Genetics:
A:Gene: GDB:AR
A:Cross-references: GDB:120556; OMIM:313700
A:Map position: Xq11-qx12
A:Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; steroid binding; transcription regulation; zinc finger
F:557-815/Domain: erba transforming protein homology <ERBA>
F:559-579/Region: zinc finger
F:595-619/Region: zinc finger

Query Match 99.3%; Score 4880; DB 2; Length 919;
Best Local Similarity 99.6%; Pred. No. 3.4e-250;
Matches 919; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 MEVGLGRVYPRPSTYRGAFQNLFSQVREVIQNGPRHPEAASAPPASLLILQQO 60
Db 1 MEVGLGRVYPRPSTYRGAFQNLFSQVREVIQNGPRHPEAASAPPASLLIL--- 57
Qy 61 QOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 120
Db 58 -OQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 116
Qy 121 POSALECHPERGCVPEGA AVASKGLPQOLPAPPDEDSAPSTLSLGLPTFPGLSSCS 180
Db 117 POSALECHPERGCVPEGA AVASKGLPQOLPAPPDEDSAPSTLSLGLPTFPGLSSCS 176
Qy 181 ADLKDILSEASTMQLQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 240
Db 177 ADLKDILSEASTMQLQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 236
Qy 241 LCKAVSVSNGLGVRALEHLSPEQLRGDCMYAPLLGVPPAVRTPCAPLAECKGSLDD 300
Db 237 LCKAVSVSNGLGVRALEHLSPEQLRGDCMYAPLLGVPPAVRTPCAPLAECKGSLDD 296
Qy 301 AGKSTEDTAETSPFKGGYTKLEGSIGCSGSAAGSGTLELFTSLYKSGALDEAAA 360

Db 297 AGKSTEDTAETSPFKGGYTKLEGSIGCSGSAAGSGTLELFTSLYKSGALDEAAA 356
Qy 361 YQSDYNYNPLALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCQRYGLASLHGAG 420
Db 357 YQSDYNYNPLALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCQRYGLASLHGAG 416
Qy 421 AAGPGSGPSAAAASSSSHTLTAEAGQLYPCPGGGGGGGGGGGGGGGGGGGGGGGEAGA 480
Db 417 AAGPGSGPSAAAASSSSHTLTAEAGQLYPCPGGGGGGGGGGGGGGGGGGGGGGGEAGA 476
Qy 481 VAPYGYTRPPOGLAGQESDFTAPDVWYPGGMVSRVPYPTCVKSEMPWMDSYSPYGD 540
Db 477 VAPYGYTRPPOGLAGQESDFTAPDVWYPGGMVSRVPYPTCVKSEMPWMDSYSPYGD 536
Qy 541 MRLETARDHVLPIIDYPPPOKTCILICGDEASGCHYGALTCGCKVFKRAAEKQYLCA 600
Db 537 MRLETARDHVLPIIDYPPPOKTCILICGDEASGCHYGALTCGCKVFKRAAEKQYLCA 596
Qy 601 SRNDCTIDKFRKNCPCRLKCKYEAGMTLGARKLKLGNLKLQEEGEASSTTSPTTEET 660
Db 597 SRNDCTIDKFRKNCPCRLKCKYEAGMTLGARKLKLGNLKLQEEGEASSTTSPTTEET 656
Qy 661 KQLFTVSHIEGECOPIFLNVLEATEPGVVCAGHDNNOPDSFAALLSSNLGELGERQLVHV 720
Db 657 KQLFTVSHIEGECOPIFLNVLEATEPGVVCAGHDNNOPDSFAALLSSNLGELGERQLVHV 716
Qy 721 KWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRFTVNSRMLYFADPLVFNRYMH 780
Db 717 KWAKALPGFRNLHVDDQMAVIOYSWMGLMVFAMGWRFTVNSRMLYFADPLVFNRYMH 776
Qy 781 KSRMYSQCVRMHLSQERFGLQITPOEFLCMKALLFSIIPVGLKNQKFFDELRMNVIK 840
Db 777 KSRMYSQCVRMHLSQERFGLQITPOEFLCMKALLFSIIPVGLKNQKFFDELRMNVIK 836
Qy 841 ELDRITACKRNKPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 900
Db 837 ELDRITACKRNKPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 896
Qy 901 EIISVQVPKILSGKVKPIYFHTQ 923
Db 897 EIISVQVPKILSGKVKPIYFHTQ 919
RESULT 2
A34721
androgen receptor A - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C:Accession: A34721
R:Govindan, M.V.
Mol. Endocrinol. 4, 417-427, 1990
A:Title: Specific region in hormone binding domain is essential for hormone binding a
A:Reference number: A34721; MUID:90258935; PMID:2342476
A:Accession: A34721
A:Molecule type: mRNA
A:Residues: 1-910 <GOV>
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:548-806/Domain: erba transforming protein homology <ERBA>
F:550-570/Region: zinc finger
F:586-610/Region: zinc finger
Query Match 97.7%; Score 4798.5; DB 2; Length 910;
Best Local Similarity 98.3%; Pred. No. 6.8e-246;
Matches 907; Conservative 1; Mismatches 2; Indels 13; Gaps 2;
Qy 1 MEVGLGRVYPRPSTYRGAFQNLFSQVREVIQNGPRHPEAASAPPASLLILQQO 60
Db 1 MEVGLGRVYPRPSTYRGAFQNLFSQVREVIQNGPRHPEAASAPPASLLIL--- 57
Qy 61 QOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 120
Db 58 -OQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQOQQO 115

QY 343 LPSTLSLYKSGADEAANAQSRDYNFNPLALAGAPPppppphPHARIKLLENPDLJ3SAWA 407
:
D8 337 TPSSLLSYKSGAVDEAAAIQNDRYINFPLALSGPPPPPPTHPHARIKLENDLDYGSAW 396
:
QY 403 AAAACRYTGDIASLHGGAAGPGSGSPSAAAASSWHITFLTAEBQLYPCGGGGGCGGG 462
:
D8 397 AAAACRYGDIALSLHGGSVAGPYGTCTRPATASSSWHTLTFTAEGOLYGP ----- 445
:
QY 463 GGGGGGGGGGGGEAGAVAPYGTTRPPGLAQGESDFTADPVWVPGGVMSRVYPSPTC 522
:
D8 446 ----GGGGGSSSDAGFPAYIGTTRPPGLAQSGEDFSASEVMVPGVVNRVPYPSPC 501
:
QY 523 VKSEMPMWDYSGYGDMRLTDARDHVLPIDYYFPPQKTCLICGDEASCHYGALTCSGS 582
:
D8 502 VKSEMPMNENSGPYGDMRLDSTRDHVLPIDYFFPPQKTCLICGDEASCHYGALTCSGS 561
:
QY 583 CKVFVKRAEKGQKYLCASNDCITDKFRKKNCPCRKRKCYEAGMTLGARKLKLGNLK 642
:
D8 562 CKVFVKRAEKGQKYLCASNDCITDKFRKKNCPCRKRKCYEAGMTLGARKLKLGNLK 621
:
QY 643 LOEEGEASTTSPTBEETQKLVSHIEGYECOPIFUNVLEATEPGVCVCAHDNNQPDSFA 702
:
D8 622 LOEEGENSAGSPTEDPSOKTMVSHIEGYECOPIFUNVLEATEPGVCVCAHDNNQPDSFA 681
:
QY 703 ALLSSLNELGERQLYHHVYKAKALPGFNHLVDQDAVLOIYSWMGLMYFMGWRSFTNVN 762
:
D8 682 ALLSSLNELGERQLYHHVYKAKALPGFNHLVDQDAVLOIYSWMGLMYFMGWRSFTNVN 741
:
QY 763 SRMLYFAPDLVFNERYMHKSVMYSCQVRMRHLSOERGNWLQITPOEFCKALKLLFSLIIPV 822
:
D8 742 SRMLYFAPDLVFNERYMHKSVMYSCQVRMRHLSOERGNWLQITPOEFCKALKLLFSLIIPV 801
:
QY 823 DGLKNQKFDELRMNYIKELDRITACKRNKPTSCSRFRFYQLTKLLDSVQPIARELHOFTF 884
:
D8 802 DGLKNQKFDELRMNYIKELDRITACKRNKPTSCSRFRFYQLTKLLDSVQPIARELHOFTF 861
:
QY 883 DLLIKSHMVSVDFPEMAAEILISVQVPKILSGKVPIYFHQTQ 923
:
D8 862 DLLIKSHMVSVDFPEMAAEILISVQVPKILSGKVPIYFHQTQ 902
:
RESULT 5

A35895
androgen receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 20-Sep-1990
C:Accession: A35895; A37255; A37908; S34398; S17198; S40626; I49501; S1201
R:He. W.W.; Fischer, L.M.; Sun, S.; Bilhart, D.L.; Zhu, X.; Young, C.Y.F.
Biochem. Biophys. Res. Commun. 171, 697-704, 1990
A>Title: Molecular cloning of androgen receptors from divergent species w
aptor cDNA probes from dog, guinea pig and clawed frog.
A:Reference number: A35895; MUID:90386642; PMID:2403358
A:Accession: A35895
A:Molecule type: mRNA
A:Residues: 1-899 <HEA>
A:Cross-references: EMBL:X53779; NID:g49966; PIDN:CAA37795.1; PID:g49967
R:Gaspar, M.L.; Meo, T.; Tosì, M.
Mol. Endocrinol. 4, 1600-1610, 1990
A>Title: Structure and size distribution of the androgen receptor mRNA in
A:Reference number: A37255; MUID:91133433; PMID:2178222
A:Accession: A37255
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-899 <GAS>
A:Cross-references: GB:M37890; NID:g191935; PIDN:AAA37234.1; PID:g191936
R:Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Willson, E.M.; French
Mol. Endocrinol. 5, 573-581, 1991
A>Title: A frameshift mutation destabilizes androgen receptor messenger R
A:Reference number: A37908; MUID:9201874; PMID:1681426
A:Accession: A37908
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-899 <CHA>

A:Cross-references: GB:856585; NID:9236048; PIDN:AA19916.1; PID:9236049
R:Faber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Both, N.J.; Trapman, J.
Blochem. J. 278, 269-278, 1991
A:Title: The mouse androgen receptor. Functional analysis of the protein and characteriz
A:Reference number: S17198; MUID:91954214; PMID:1883336
A:Accession: S34398
A:Molecule type: DNA
A:Residues: 1-899 <FAB>
A:Cross-references: EMBL:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A:Accession: S17198
A:Molecule type: mRNA
A:Residues: 1-899 <FAB>
A:Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
R:He, W.W.; Kumar, M.V.; Tindall, D.J.
Nucleic Acids Res. 19, 2373-2378, 1991
A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen i
A:Reference number: S40626; MUID:91252278; PMID:2041777
A:Accession: S40626
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 366-413 <HEW>
A:Cross-references: EMBL:X53779
R:Gaspar, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991
A:Title: A single base deletion in the *trm* androgen receptor gene creates a short-lived
A:Reference number: I49501; MUID:92020902; PMID:1924321
A:Accession: I49501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-899 <RES>
A:Cross-references: GB:M37890; NID:9191935; PIDN:AAA37234.1; PID:9191936
C:Genetics:
A:Introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 848/3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:1-536/Domain: regulatory status predicted <REG>
F:537-795/Domain: regulatory status predicted <REG>
F:539-559/Region: erba transforming protein homology <ERBA>
F:575-599/Region: zinc finger
F:650-899/Domain: hormone binding #status predicted <LIG>

Query Match 85.0%; Score 4176; DB 2; Length 899;
Best Local Similarity 84.1%; Pred. No. 4.8e-213;
Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;
QY 1 MEVQLGLGRVYPRPSKTYRGAFONLQSVREVIONPGPHRPAASAPPGASLLLLQQ 60
Db 1 MEVQLGLGRVYPRPSKTYRGAFONLQSVREVIONPGPHRPAASAPPGASLLLLQQ 60
QY 61 QQQ 119
Db 55 -----QQ 119
QY 120 QPQSALECHPGRGCVPPGGAARAKGLPOOLPAPDEDDSAAPSTLSLLGPTFGLSSC 179
Db 97 QQQAASEGHPESSCLPEPGATAPKGLPOOPPPAPDDDDSAAPSTLSLLGPTFGLSSC 156
QY 180 SADLKILSEASTMQLLQ-----QQQQQAVSEGSSSGRAREASGAPTSSK 224
Db 157 SADIKDILNEAGTMQLLQOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 215
QY 225 DNYLGGTSTSDNAKELCAVSMGLGVLEHLSPGQRLGDCMYAPLLGVPPAVRPT 284
Db 216 DSYLGGNSTSDSAKELCAVSMGLGVLEHLSPGQRLGDCMYASLLGGPPAVRPT 275
QY 285 PCAPLAECKSLDDSGAKSTEDTAETSPFKGTYKGLGESLGCSSGAAGSSGTLLEP 344
Db 276 PCAPLPECKGLPDEPGKSTEDTAETSPFKGTYKGLGESLGCSSGAAGSSGTLLEP 335
QY 345 STLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 404
Db 336 SSLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 395

QY 405 AAOCRYGDLASLHAGAGCGSPSAAASSSWHTLTAEQGLYXPCGCGGGGGGGGGG 464
Db 396 AAOCRYGDLGSLHGGVAGSPSTGPPATSSSWHTLTAEQGLYXPCGCGGGGGGGGGG 464
QY 465 GGGGGGGGGGGEAGAVAPYGYTRPPQGLAGQSDFTAPDVWYPGGMSRVPPSPPTCVK 524
Db 443 --GGGGGSSPSDAGVPVGYTRPPQGLTQSDYSASEVWYPGGVNRYPPSPNCVK 500
QY 525 SEMCPWMDSYSGYGDNRLETARDHVLPIIDYFFPQKTLICGDEASGCHYGALTCGSK 584
Db 501 SEMGPWMENTSGYGDNRLEDTRDHLPIIDYFFPQKTLICGDEASGCHYGALTCGSK 560
QY 585 VFFKRAAEQKQKYLCAASRNDCTIDFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQ 644
Db 561 VFFKRAAEQKQKYLCAASRNDCTIDFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQ 620
QY 645 EEGEASSTTSPTEETQKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQPDFAAL 704
Db 621 EGENSNAGSPTEDPQKMTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQPDFAAL 680
QY 705 LSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGLMVFMGHRSTNVNSR 764
Db 681 LSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGLMVFMGHRSTNVNSR 740
QY 765 MLYFAPDLVFNRYMHKSRMYSCQVVRHLSQEFGLQITPQEFCLMKALLFSIIPVDG 824
Db 741 MLYFAPDLVFNRYMHKSRMYSCQVVRHLSQEFGLQITPQEFCLMKALLFSIIPVDG 800
QY 825 LKNQFFDELRYNIKELDRIIACKRNKPTSCSRFFVOLTLLKLSVQPIARELHOFITDL 884
Db 801 LKNQFFDELRYNIKELDRIIACKRNKPTSCSRFFVOLTLLKLSVQPIARELHOFITDL 860
QY 885 LKSHMSVDPEMMAEIIISVOVKILSGVKPIYFHTQ 923
Db 861 LKSHMSVDPEMMAEIIISVOVKILSGVKPIYFHTQ 899
RESULT 6
I51330
androgen receptor - common canary (fragment)
C:Species: Serinus canaria (common canary)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C:Accession: I51330
R:Nastiuk, K.L.; Clayton, D.F.
Endocrinology 134, 640-649, 1994
A:Title: Seasonal and tissue-specific regulation of canary androgen receptor message
A:Reference number: I51330; MUID:94130808; PMID:8299561
A:Accession: I51330
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <NAS>
A:Cross-references: GB:L25901; NID:9414733; PIDN:AA17402.1; PID:9414734
C:Genetics:
A:Gene: AR
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:1-251/Domain: erba transforming protein homology (fragment) <ERBA>
Query Match 34.1%; Score 1676; DB 2; Length 344;
Best Local Similarity 90.4%; Pred. No. 1.5e-81;
Matches 311; Conservative 20; Mismatches 13; Indels -0; Gaps 0;
QY 569 EASGCHYALTCGSKCVFFKRAAEQKQYLCAASRNDCTIDFRKNCPSCLRKCYEAGM 628
Db 1 EASGCHYALTCGSKCVFFKRAAEQKQYLCAASRNDCTIDFRKNCPSCLRKCYEAGM 60
QY 629 TLGARKLKLGNLKLQEEGEASSTTSPTEETQKLTVSHIEGYEQPIFLNVLEAIEPGV 688
Db 61 TLGARKLKLGNLKLQADDDIEGASSSSSTEOPAKLVMTRIDGYEQPIFLNVLEAIEPGV 120
QY 689 VCAGHDNNQPDFAALLSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGL 748
Db 121 VCAGHDNNQPDFAALLSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGL 180

[illegible]

Db 233 GPLLKQPRALGGTAAGGAAPVASGAAA-----GGVALVPKEDSRFSAPRVSLA--- 282
QY 252 GVEALEHLSPEQLRG-----DCMYAPLLGVPPAVRPTPCAPLAECGSLDSDSAGKST-- 305
Db 283 --EQDAPVAPGKSPPLATSVVDFFIHVPILPLNHLAFATRTQLLE--GESYDGGAAASPF 338
QY 306 -----EDTAESYSPKGG-----YTKLEGESLGCSSAAAGSGTLELPSTLSLYKSGA 354
Db 339 VPQGSFASSTPVAGGDFDCTYPPDAEPK-----DDAFPLYGDFQ--PPALKIKEE 391
QY 355 LDEAAAYQSRDY-----NFP--LALAGPPPPPPHPPHARKLENPLDLYGSANAAAA 406
Db 392 AAEAAARSPTLYVAGANPAAPDFQLAAPPPPSLPP-----RVPSRP--GEA----- 438
QY 407 QCRVGLASLHAGAGAGPGSGPSAAASSSWH---TLFTAE-----EGOLY-PCGGGGG 457
Db 439 -----AAVASPGSASVSSSSSGSTLECLYKAEGAPPOGPFAPLCKPPGA 486
QY 458 GGGGGGGGGGGGGGGGGGAGAVPYGYTRPPQGLAGQESDFTAPDVMYVGMYSR--- 514
Db 487 GACLLPRDGLPSTASGAAGAAPALY-----PTLGLNG-----LPOLGYQAAVLKEGLP 536
QY 515 ---VPDPTCVKSEMPWMDSYSGPYGDMRLTARDHVLPIDYFPP--POKTLICGDE 569
Db 537 QVYTPY-----LNLYRPDSEASQSP-----QYSFESLPKICLICIGDE 574
QY 570 ASGCHYGALTCGCKVFFKRAEGKOKYLCASRNDCTIDKFRKNCPSCLRKYEAGMT 629
Db 575 ASGCHGVLTCGCKVFFKRAEGQHNYLCAGRNDCIYDKIRKNCACRLKRCQAGW 634
QY 630 LGARKLKLNLKLOEGEASSTTPT--EETTKLTVSHTEGECQIFLNLEATEPG 687
Db 635 LGGRKFKTKNVRMRALDAVALPOVGIPIPNESQITSPSQEQLPLPLNLMSTEDP 694
QY 688 VVACAGHNNQDPSFALLSLNELGERQLVHVYKAKLPGRNLHVDQMAVYQYSWMG 747
Db 695 VIYAGHNTKPTSSLSLNLQGERQLLSVVKWSKSLPGRNLHDDQITLLQYSWS 754
QY 748 LMVFAMGWSFTNVRMLYFAPDLVFNEXYRMHKSVMYSCQVRMHLISQFEGWQITPQE 807
Db 755 LMVFGLGWSYKRVHVSQMLYFAPDLINQRMKSSYSUCLTMWQIPQEFVKLOVSQEE 814
QY 808 FLCMKALLFSIIPVDGLKNKFFDELRMNYIKELDRIAKRNKPTSCSRFFVQLTKL 867
Db 815 FLCMKVLLNNTIPLGLRSQSEEMRSSYIRELKAIGLRQKGVVSSSQRYQITKLL 874
QY 868 DSVQPIARELHOFTDILLIKSHMYSDVPPENMAELISVQVPKILSGVKPIYFH 921
Db 875 DNLHDLVQLHLIYCLNTFIQSRALVSVEPPENMSEVIAAQLPKILAGMVKPLLFH 928

RESULT 9
QRHUP
progesterone receptor form B - human
N:Alternate names: hpr
C:Species: progesterone receptor form A
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
R:Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gronemeyer, H.; Chambon, P.
EMBO J. 9, 1603-1614, 1990
A:Title: Two distinct estrogen-regulated promoters generate transcripts encoding the two
A:Reference number: S09971; MUID:90228361; PMID:2328727
A:Accession: S09971
A:Molecule type: mRNA
A:Residues: 1-933 <RAS>
A:Cross-references: EMBL:X51730
R:Kastner, P.
submitted to the EMBL Data Library, February 1990
A:Reference number: S12464
A:Accession: S12464
A:Molecule type: mRNA
A:Residues: 1-343, 'T', 345-933 <KA2>

A:Cross-references: EMBL:X51730; NID:935651; PIDN:CAA36018.1; PID:935652
R:Mirzahi, M.; Atger, M.; D'Auriol, L.; Loosfelt, H.; Meriel, C.; Fridlansky, F.; Gul
Biochem. Biophys. Res. Commun. 143, 740-748, 1987
A:Title: Complete amino acid sequence of the human progesterone receptor deduced from
A:Reference number: A03245; MUID:87184565; PMID:3551956
A:Accession: A03245
A:Molecule type: mRNA
A:Residues: 1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <MIS>
A:Cross-references: GB:M15716; NID:9189934; PIDN:AAA60081.1; PID:9189935
C:Genetics:
A:Gene: GDB:PCR
A:Cross-references: GDB:119493; OMIM:264080
A:Map position: 11q22.1-11q22.3
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormo
F:1-933/Product: progesterone receptor form B #status predicted <MA>
F:165-933/Product: progesterone receptor form A #status predicted <MA2>
F:565-829/Domain: erba transforming protein homology <ERBA>
F:567-587/Region: zinc finger CCCC motif
F:603-627/Region: zinc finger CCCC motif
F:681-933/Domain: steroid binding #status predicted <STB>
F:41/Binding site: phosphate (Thr) (covalent) #status predicted
F:227,232,552,793/Binding site: phosphate (Ser) (covalent) #status predicted
F:329,374,601/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 25.7%; Score 1262; DB 1; Length 933;
Best Local Similarity 34.3%; Pred. No. 3.2e-59;
Matches 347; Conservative 123; Mismatches 326; Indels 216; Gaps 33;

QY 38 GPRHPEAASAAP-----PGA-----SLLLLQQQ000000 66
Db 8 GPRAPHVAGGPPSPVGLLCPRAAGFPFGSQTSLPVSATPISLDGLLFFPRPCQG 67
QY 67 QQQQQQQQQQQQQQQQETSPRQ000000GDSGQAHRRGPTGYL--VLDEEQPQSPQSA 124
Db 68 DPSDEKTDQDQSLSDVEGAYRAEATRGAGGSSSPKESGLDLSVLDILLAPSGPGS 127
QY 125 LECHPERGCVPEPAAVAASKG--LPQOLPAPPEDESSAAPTSLILGTFP-----GL 176
Db 128 -----QSPSPACEVTSSWCLFGPELP-----EDPAPATQTVLSPLMSRSGCKVGD 174
QY 177 SSCSADLKDIUSE--ASTMQL-----QQQQQAVS--EGSSSGRAREAG 218
Db 175 SSGTAAAHKVLPRGLSPARQLLPASESPHWSGAPVPSQAAAVEEEDSESESAG 234
QY 219 APTSSKDNVLGTSITSDNAKELCKAYSVSNGLG-----VEALEHLSPC 262
Db 235 PLLKGPALGGAA--AGGGAACPPGAAAGGVALVPKEDSRFSAPRVALVEQADPAWG 292
QY 263 BOLRG---DCMYAPLLGVPPAVRPTPCAPLAECGSLDSDSAGKSTEDTAESYSPKGY 318
Db 293 RSLPATTVMDFIHVPIL-----PLNHALLAARTQLLEDES-----YDGGAGAA 336
QY 319 TKLEGESLGCSS--AAAGSSGTLELP-----STLSLY-----KSGALD 356
Db 337 SAFAPPRSSPCASSTPVAVGDFDPCAYPPDAEPKDDAYPLYSDFQPALKKEEEGA-- 394
QY 357 EAAAYQSRDY-----NFPALAGPPPPPPHPPHARKLENPLDLYGSANAAAA 406
Db 395 EASARSPRSYLVAGANPAAPDFPL--GPPPLPP-----RAT 430
QY 407 QCRVGLASLHAGAGAGPGSGPSAAASSSWH---TLFTAE-----EGOLYPCGGGGG 458
Db 431 PSRPG-----AAVTAAPASASVSSSSSGSTLECLYKAEGAPPOGPFAPPCAPGA 485
QY 459 GGGGGGGGGGGGGGGGGGAGAVPYGYTRPPQGLAGQESDFTAPDVMYVGMYSR--VPY 517
Db 486 SGCLLPRDGLPSTASGAAGA-APALY--PALGLNG-----LPOLGYQAAVLKEGLPQ 536
QY 518 PSTCVKSEMPWMDSYSGPYGDMRLTARDHVLPIDYFPP--POKTLICGDEASGCHY 575
Db 537 VYPPYL-NLYRPDSEASQSP-----QYSFESLPKICLICGDEASGCHY 579

Query Match 24.8%; Score 1218; DB 2; Length 786;
Best Local Similarity 33.4%; Pred. NO. 5.5e-57;
Matches 325; Conservative 128; Mismatches 259; Indels 260; Gaps 30;

progesterone receptor B form - mouse

C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999
C:Accession: A39596; I49111
R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.
Biochemistry 30, 7014-7020, 1991
A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA encoding a rat mineralocorticoid receptor
A:Reference number: A39596; MUID:91299759; PMID:2069958
A:Accession: A39596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-923 <SCH>
A:Cross-references: GB:M68915; GB:J05333; NID:G200471; PIDN:AAA39971.1; PID:G200472
R:Hagihara, K.; Wu-Peng, S.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the mouse mineralocorticoid receptor gene
A:Reference number: I49111; MUID:95100931; PMID:7802637
A:Accession: I49111
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <HAG>
A:Cross-references: EMBL:U12644; NID:G639916; PIDN:AAA66067.1; PID:G639917
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger
F:555-819/Domain: erba transforming protein homology <ERBA>
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

Query Match 24.5%; Score 1205; DB 2; Length 923;
Best Local Similarity 32.2%; Pred. No. 3.2e-56;
Matches 337; Conservative 119; Mismatches 301; Indels 288; Gaps 36;

QY 35 ONFGPRHPEAASAPP--GASILLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ-- 86
DB 7 KDPQVLTGASPSPHIGSPLL-----ARLDGFGQSGHSDYSSVSPISLD 57
QY 87 -----RQOQQQQQGGDGSPPQA-----HRRGPTYG-----LVLD 113
DB 58 GLLFPSCRCRGPDPGKTGQDQSLSDVEGAFSGVEATHREGGRNRPPEKDSRLDSDVLD 117
QY 114 EQQPSQPSALECHPERGCVPEPFGAASAKGLPQPLPAPDDEDSAPSTLSLIGTFF 173
DB 118 SLLTPSGPE---QSHAS---PPACEITSWCLFGFELP-----EDRSPVPATKGLSP-- 164
QY 174 PGLSSCSADLKDLSEASTMQLLQOQQQEAQVSEGGSSGRARASGAPTSSKDNLYGGTST 233
DB 165 -----LMSREIKVGDQSGTGRQ----- 183
QY 234 ISDNAELCKAVSMGLGVEALEHLSPEQL---RGDCMYAPLLGVPVAVRTPCAPLA 290
DB 184 -----KVLPGK-----LSPPRLLLPTSGSAHWPGAGVKPS---PQPA-- 219
QY 291 ECKGSLDSDSAGKTEDTAEYSPKGGYTKGLEGESIG---CSGSAAGSSGTLELPSTL 347
DB 220 ---GEVEDS-GLTEGSA--SPLKSKPRALGEGTGGGGVAAAFSAAPGGVTLVPKED 273
QY 348 SLYKSGALD-----EAAAYQSDRYNFPN-----A 372
DB 274 SRFSAVPSLEQDSPAPGRSPPLATTVDFTHVPLPLNHALLAARTROLLEGESYDGA 333
QY 373 LAGPPPPPPPP-----HPARKLEN-----PLDYGSAWAAAAACRYGDLA 414
DB 334 TAGPFCPPRSPASPTVPVRGDFPDCTYPLEGDKEDVFL-----YGDQ 379
QY 415 S-----LHGAGAAGPGSGSP-----SAAASSWHLTFTAEQGLYGPCCGGGGGGGG 462
DB 380 TPLGLKKEEEGADAA---VRSPPYLSAGASSTTFDFPLAPAPQAAPASRRPGEAAVAG 436
QY 463 GGGGGGGGGGGGGA-----CAVAPYGYTRP-----QGLAQESD 499
DB 437 GPSSAAVSPASSSGSALFECILYKAEAPPTQGSFALP--CKPPAAACLLPRDSLPAPGT 495
QY 500 FTAPDWWPGGMVSRVPSPSTCVKSEMGPMWDSYSGPYGDMRLLETARDHVLPP--IDYF 557
DB 557 ----- 557

DB 496 AAPATYQPLGL--NGLP-----QLG-----TQAAVLKDSLPQVPPYLYNLR 536
QY 558 P-----PQKTCICGDEASCHYGALTGCGSKCVFFKRAAEGKQKYLCA 602
DB 537 PDSEASQSPQGFDSLPQKICLICGDEASCHYGVLTCGSKCVFFKRAEAGHNYLCAGR 596
QY 603 NDCTIDFRNRKNCPSCLRYEAGMTLGARKLKKLNKLQE--EGEA--SSTTSPT 658
DB 597 NDCIVDKIRRNKCPACRLKCCQAGVGLGKFKFKKVRMRTLDGVALPQSGVLPNES 656
QY 659 --TTOKLTVSHLEGYECOPILNLEALEIPGVVCGAGHNNQPDPSFAALLSSLNELGERQL 716
DB 657 QALSORITFSNQELQVPPPINLMSIEPDVYVAGHNTKPDTSSTSLTSLNOLGERQL 716
QY 717 VHVVKAKALGFRNLHVDVDDQMAVQIYSWMLGVFANGWRSFTNNVSRMFLYFAPDLVFN 776
DB 717 LSVVWKSLSLPGFRNLHIDDQITLIQIYSWMSLMVFGWRSYKHVSQML7FAPDLILNE 776
QY 777 YRMHKSRYSCVVRMHLSEQFGWLOITPOEFLCMKALLFIIPVDGLKNQKFFDELRM 836
DB 777 QRMKELSFYSLCTVMQIPQEFVKLVQVTHEEFLCMKVLILLNTIPIELRSQSOFEMRS 836
QY 837 NYIKELDRIIACKRNKPTSCRRFYQLTKLDSVQIARELHQFTFDLLIKSHMVSVDFP 896
DB 837 STIRELIKAIGLRQKGVVPTSORFYQLTKLDSLHDLVKQLHLYCLNTFIQSRITLAEFP 896
QY 897 EMMAELISVQVPEKILSGKVKPIYFH 921
DB 897 EMMSEVIAQLPKILAGVMVKPLLFH 921

RESULT 13
A41401
mineralocorticoid receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-Sep-1999
C:Accession: A41401
R:Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
Mol. Endocrinol. 3, 1877-1885, 1989
A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA
A:Reference number: A41401; MUID:90114194; PMID:2558305
A:Accession: A41401
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <PAT>
A:Cross-references: GB:M36074; NID:G205340; PIDN:AAA41583.1; PID:G205341
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:602-877/Domain: erba transforming protein homology <ERBA>
F:604-624/Region: zinc finger
F:640-664/Region: zinc finger

Query Match 22.2%; Score 1092; DB 2; Length 981;
Best Local Similarity 32.0%; Pred. No. 3.2e-50;
Matches 310; Conservative 119; Mismatches 306; Indels 234; Gaps 34;

QY 77 QOQQOQETSPPR---QOQQOQGGDGSQAHRRGPTGYLVLDDEEQSPQPOSA----- 124
DB 121 QOQQOQSLSPTKIYQNMQLVKYKENGHRSTLS--AMSRPLRSFMPDAAAMNGALR 178
QY 125 -----LECHPERGCVPEP---GAANAASKGL-----PQQLPAPDEDDSA 162
DB 179 AIVKSPIICEKSSVSSPLNMASVCSVPVGINSMSSSTTSFGSPVHSPFTQGTSLTCS 238
QY 163 PST-----LSLLGPTFFGLSSCSADLKDLSEASTMOLLOQ 198
DB 239 PSVNRGSRSHSPHASNVGSPSLSSPMKSISSPPSHCS--VKSPYSSPNVPLRSS 296
QY 199 QQOQEA-----VSEGSSGRAREASGAPTSSKDNLYGGTSTISDNALCKAVSVMG 250
DB 297 VSSPANLNNSRCSVSSPNNNRSSTLSSTASTVSGIS--SPISNAFYATSGAGAGAG 354
QY 251 LGVEALEHLSFG---EQLRGDCMYAPLLGVPVAVRTPCAPL-----AECGSLDD 299

Db 355 ---AIDVSPDTHKGAHVPFKTEVEKASNGVGTPLNIYQYIKSEPDGAFSS 410
QY 300 SAGKSTEDATARYSPFKGYTKGLEBSLGCSSAAAGSGTLELPSTLSLYKSGALDEAA 359
Db 411 CLGNSK-IPSPSPFVPIKQ--ESSKHSCSGASFGNPTVNPFPMDGSGYFS-FWDD-- 464
QY 360 AYQSRDYNFPLALAGPPPP-----PPPPHARIKLENPLDYGSAMAAAAQRCYGL 413
Db 465 ----KDYISLS-GILGPPVPCFDCSDSAFP--VGIKQEPDGS-----YYPE 506
QY 414 ASLHGAACGPGSGSFAAASWHWLTAEAGQLYKPGCGGGGGGGGGGGGGGGGGGG 473
Db 507 ASIPSSAIVGNVG-----GQSFHY----- 526
QY 474 GGGGAGAVAPYGYTRPPQGLAGQSDFTAPDVWYPGMVSRVYPSPTCVKSEMGPWMS 533
Db 527 ---RIGAQTISLSRSPDQSFQH-----LSSFP-PVNTLVES-----WK-- 562
QY 534 YSGPYGDMRLTARDHVLPIDYFP-----PQKTLICGDEASGCHYG 576
Db 563 ----PHGD--LSSRRSDGYPVLEYIPENVSSTLRSVSTGSSRPSKICLVCGDEASGCHYG 617
QY 577 ALTGCGSKVFFKRAAEGKQKYLCAASNDCTIDKFRKNCPCSLRKYEAGMTLGARKLK 636
Db 618 VWTGCGSKVFFKRAVEGQHNLYLCAGNRDCTIDKIRKNCPCACQKCLQAGMNLGARKSK 677
QY 637 KLGNLK-LQEE-----GEASSTTSPTTEET-----QKLTVSHIEGYEQP 675
Db 678 KLGLKGLHEEQPQPPPPPPQSPPEGTTYIAPTKEPSVNSALPQLTSTITH-----ALTP 733
QY 676 IFNLVLEATEPGVVCAGHDNDPDSFALLSSLNGLERQQLVHVYKAKALPGRNLHYD 735
Db 734 SPAMILENLEPVTAGYDINSKPDFAESLLSTLNRLAAKQMIQVVKAKVLPFGKNLPE 793
QY 736 DQNAVTOYSWMGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYMHKSMYSCQVRMHL 795
Db 794 DQITLIQYSWMGLSSFALSWSRYKHTNSQLLYFAPDLVFNRYMHKSMYSCQVRMHL 853
QY 796 QEFGLWLTPOFLCQKALLLSIIPVGLKNQKFFDELNRNYIKELDRITACKRNKPTS 855
Db 854 LQFVRLQLTFFEYSIMKVLLLSLTPKDKLQSAFAEEMRTNYIKELRKMVT---KCPNS 910
QY 856 CS---RRFYQLTKLSDVQPIARELHOFTFLLIKSHMVSVDPEMMAEIIISVQV 912
Db 911 SGOSWQRYQLTKLSDVQPIARELHOFTFLLIKSHMVSVDPEMMAEIIISVQV 970
QY 913 GKVKPIYFH 921
Db 971 GNAKPLIYFH 979

RESULT 14
A29513
N:Mineralocorticoid receptor - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D.E.
Science 237, 268-275, 1987
A:Title: Cloning of human mineralocorticoid receptor complementary DNA: structural and
A:Reference number: A29513; MUID:87263386; PMID:3037703
A:Accession: A29513
A:Molecule type: mRNA
A:Residues: 1-984 <ARR>
A:Cross-references: GB:M16801; NID:g187460; PIDN:AAA59571.1; PID:g307166
C:Genetics:
A:Gene: GDB:MLR
A:Cross-references: GDB:120188; OMIM:264350
A:Map position: 4q31-4q31
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger

F:601-880/Domain: erba transforming protein homology <ERBA>
F:603-623/Region: zinc finger
F:639-663/Region: zinc finger

Query Match 22.0%; Score 1078.5; DB 2; Length 984;
Best Local Similarity 32.8%; Pred. No. 1.6e-49;
Matches 300; Conservative 101; Mismatches 254; Indels 259; Gaps 30;

QY 98 SPQARRRGPTGYL-----VLDEEQP-SQPOSALCEHPERCVCPEP--GAVAASK 145
Db 238 SPANRGRSHSHPAHASNVGSPLSPLSSMKSSISSPSHCSVKSVPSSNNVTLRSSV 297
QY 146 GLPQQL-----PAPDEDD-----SAAPSTL-SLLGP-----TFPGLSSCADLKD 185
Db 298 SSPANTNNRCVSSPSNTNRRSTLSSPAASTVSGTCSVNNAFSYTASGTAGSSTLTD 357
QY 186 ILSEASTMQLLOQ-----OQEAIVSEGSSSGRA-----REASGAPT-SKENYLGCT 231
Db 358 VVPSPTQKGAQVPPFKTEEVESAINGVGTQNLIVQYIKPEPDGAFSS--CLGNN 414
QY 232 STISDNAKELCAVSVSMGLVGEALHLSPEQLRGDCMYAPLLGVPPAVAPRPTCAPLAE 291
Db 415 SKINDS-----SFSVPIKQESTKHSCSGTSTFKGN-----PTVNPFP----- 451
QY 292 CKGSLDDDSAGKSTEDTAEY--SPFKGGYTKLEGESLGCSSGSAAGSSGTLELPSTLSL 349
Db 452 ----FMGYSYFMDKDYISLGLGPPVPFGDG--NCEGS----- 487
QY 350 YKSGALDEAAAYQSRDYNYFLALAGPPPPPPPHPHARIKENPLDYGSAMAAAAQCR 409
Db 488 -----GFPVGIKQEP-----DDGS----- 501
QY 410 YGDLASLHCAGAGCGSGSPSAAASSSWHTLFTAEAGQLYKPGCGGGGGGGGGGGGG 469
Db 502 YYPEASIPSSAIVGNVG-----GQSFHY----- 525
QY 470 GGGGGGAGAVAPYGYTRPPQGLAGQSDFTAPDVWYPGMVSRVYPSPTCVKSEMGP 529
Db 526 -----RIGAQTISLSRSDQSFQH-----LSSFP-PVNTLVES----- 559
QY 530 WMSYSGPYGDMRLTARDHVLPIDYFP-----PQKTLICGDEASG 572
Db 560 WKS-----HGD--LSSRRSDGYPVLEYIPENVSSTLRSVSTGSSRPSKICLVCGDEASG 612
QY 573 CHYGALTGCGSKVFFKRAAEGKQKYLCAASNDCTIDKFRKNCPCSLRKYEAGMTLGA 632
Db 613 CHYGVVTCGSKVFFKRAVEGQHNLYLCAGNRDCTIDKIRKNCPCACQKCLQAGMNLGA 672
QY 633 RKLKLGKLNK-LQEEGEASS-----TTSPTTEET-----QKLTVSH 667
Db 673 RSKKLGKLGITHEEQPQPPPPPPPPQSPPEGTTYIAPAKEPSVNTALVPLQSTISR 732
QY 668 LEGYECOPIFNLVLEATEPGVVCAGHDNDPDSFALLSSLNGLERQQLVHVYKAKALP 727
Db 733 ----ALTPSPVWLENLEPELVYAGYDINSKPDFAESLLSTLNRLAAKQMIQVVKAKVLP 788
QY 728 GFRNLHVDDQMAVIQYSWMGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYMHKSMYSCQ 787
Db 789 GFKNLPLEDQITLIQYSWMGLSSFALSWSRYKHTNSQLLYFAPDLVFNRYMHKSMYSCQ 848
QY 788 CVMRHLHSEBQWLOITPQFLCQKALLLSIIPVGLKNQKFFDELNRNYIKELDRIT 847
Db 849 COGMHQISLOFVRLQLTFFEYIMKVLLLSLTPKDKLQSAFAEEMRTNYIKELRKMVT 908
QY 848 CKRKNPTSCRRFVQLTKLSDVQPIARELHOFTFLLIKSHMVSVDPEMMAEIIISVQV 907
Db 909 KCPNNSQSWQRYQLTKLSDVQPIARELHOFTFLLIKSHMVSVDPEMMAEIIISVQV 968
QY 908 PKILSGKVKPIYFH 921
Db 969 PKVESGNAKPLIYFH 982

RESULT 15

QRTG
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1988 sequence.Revision 31-Mar-1988 #text_change 22-Jun-1999
 C:Accession: A24194; S02475; A27284; S33888; S33891
 R:Mesfeld, R.; Rusconi, S.; Godowski, P.J.; Maler, B.A.; Okret, S.; Wikstrom, A.C.; Gus
 Cell 46, 389-399, 1986
 A:Title: Genetic complementation of a glucocorticoid receptor deficiency by expression c
 A:Reference number: A24194; MUID:86272086; PMID:3755378
 A:Accession: A24194
 A:Molecule type: mRNA
 A:Residues: 1-795 <NID>
 A:CROSS-references: GB:M14053; NID:g204271; PID:AAA41203.1; PID:g204272
 R:Severne, Y.; Wieland, S.; Schaffner, W.; Rusconi, S.
 EMO J. 7, 2503-2508, 1988
 A:Title: Metal binding 'finger' structures in the glucocorticoid receptor defined by sit
 A:Reference number: S02475; MUID:89052664; PMID:3191912
 A:Accession: S02475
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 440-539 <SEV>
 R:Chang, C.; Kokontis, J.; Chang, C.T.; Liao, S.
 Nucleic Acids Res. 15, 9603, 1987
 A:Title: Cloning and sequence analysis of the rat ventral prostate glucocorticoid recept
 A:Reference number: A27284; MUID:88067783; PMID:3684608
 A:Accession: A27284
 A:Molecule type: mRNA
 A:Residues: 1-97, 'D', '99-225, 'G', '227-259, 'D', '261-344, 'T', '346-515 <CHA>
 A:CROSS-references: GB:Y00489; NID:g56324; PID:CAA68545.1; PID:g56325
 R:Gearing, K.L.; Gustafsson, J.A.; Okret, S.
 Nucleic Acids Res. 21, 2014, 1993
 A:Title: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from da
 A:Reference number: S33888; MUID:93261843; PMID:8493115
 A:Accession: S33888
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 68-97, 'D', '99-104 <GEA>
 A:CROSS-references: EMBL:X69666
 A:Accession: S33891
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 68-92, 'D', '99-104 <GE2>
 A:CROSS-references: EMBL:X69669
 A:Comment: This sequence contains five potential translation initiators: 1-Met, 28-Met,
 d is initiated from 1-Met.
 C:Superfamily: glucocorticoid receptor; erba transforming protein homology
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
 F:75-96/Region: glutamine-rich
 F:438-692/Domain: erba transforming protein homology <ERBA>
 F:440-460/Region: zinc finger CCCC motif
 F:476-500/Region: zinc finger CCCC motif

Query Match 21.7%; Score 1065; DB 1; Length 795;
 Best Local Similarity 32.0%; Pred. No. 6.7e-49;
 Matches 314; Conservative 110; Mismatches 268; Indels 288; Gaps 35;
 QY 20 RGAFONLFSYR---EVIONPGRPHRPAASAPPGASLLLL-----QQQQQQQQQQQ 68
 DB 24 RGSVDFYKSLRGATVKVSSASSPSVAASQADSKOORILLDFSGKSTSNVQORQQQQQ 83
 QY 69 QQQQQQQQQQQQQQQQETSP-----RQQQQQQQED-GSPOAHR---RGPTGLVL 112
 DB 84 QQQQQQQQQQQQQQQQGLSKAVSLMGLVMTETKVMGNDLGYQQQGLSGSETDFRL 143
 QY 113 DE-----EQPQSQPSALECHPERGCPGPAVAASKGLPQOLPAPPDEDDSAAPSTLS 167
 DB 144 EESIANLNRTSVENPKSSTSATGC-----ATPTEKE----- 176
 QY 168 LIGPTFGGLSCSADLKILSEASTMQLLQQQQQQEAVSESSSGRAREASGAPTSSKDN 227
 DB 177 -----FPKTH-----SDASS-----EQQNRKSTQTNGG-----SVKLY 205

QY 228 LGGTSTISDNAKELCKAVSVSMGLGVLEALHLSLPGQLRDCMAYPLGLGVPVAVRTPCA 287
 DB 206 PTDQSTF-----DLKDLFSAG-----SPSKDTNESPWRSDDL-----IDENLLS 246
 QY 288 PLA-----ECKGSLDDDSAG--KSTEDTAESP-----FKGG 317
 DB 247 PLAGEDDFLEGNWEDCKPLILPDKPKIKDTGDTLSSPSSVALPOVKTEKDFIEL 306
 QY 318 YTKG-LEGESLG---CSGSAAGSSGTLELPSTLS-----LYKSGA-----LDAAAY 361
 DB 307 CTGPVKEKELGPVYCO---ASFSGTNIIGKMSAISVHGVSSTGGOMYHYDMNTASLS 362
 QY 362 QSRDYNNPFLALAGPPPPPPPPHARIKENPLDYSANAAAAACRYGULASLHGAGA 421
 DB 363 QOOD--QKPVENVIPP-----VGSN-----W-----NRQO----- 388
 QY 422 AGPGSGSPSAASSSHWHLFTAEEGQLYVPCGGGGGGGGGGGGGGGGGGGGGGGAGAV 481
 DB 389 ---GSGEDSLTSL-----GALNFP-----GRSV 408
 QY 482 APYGYTRPPQGLAGQESDFTAPDVWYVPGMVSRVYPSPTCVKSEMPWMDSYSGPYGDM 541
 DB 409 FSNGYSSP-----GMRPDVSSP-----PS-----SSAATG-- 434
 QY 542 RLETDARDHVLIDYFPQKTCCLICDEASCHYGALTCGCKVFFKRAAEGKOKYLCA 601
 DB 435 -----PPKICLVCDEASCHYGVLTCGCKVFFKRAVEGQHNYLCAG 478
 QY 602 RNDCTIDKPRKNCPSRLKCYEAGMTLGARKLKLKLNKLOEGEASSTTSPTEETQ 661
 DB 479 RNDCTIDKIRKNCPCRYKRCLOAGMNLKARKTK-----KIKIQOATAGVSODTSEN 534
 QY 662 KLTVSHIEGYECOPFLNVLNLEAIEPGVVCAGHDNNOPDFAALLSSLNELGEROLVHWK 721
 DB 535 NKTIVPAALPOLPTPLVSLLEVEIEPEVLYAGTSSVPSAWRIMTTLNMLGGROVIAVK 594
 QY 722 WAKALPGFRNLHVDQMAVIOYSWMGLMVFAMGRSFTNNSRMLYFAPDLVFNERYMHK 781
 DB 595 WAKAILGLNHLDDOITLLOYSWMFLMAFALGWSYRQSSGNLICFAPDLIINEORMSL 654
 QY 782 SRMYSOCVEMRHLISQEFGLWQITPOEFLCKALLLFTIIPVDGLKNOKFDELMMYIKE 841
 DB 655 PCMYDQCKHMLFVSELOQLQVSYBEYLCMKTLLLSLSSVPKREGLKSQELFEIRMTYKE 714
 QY 842 LDRIACKKNPTSCSRREYQTLTKLSDVQPIARELHQFTFDLLIKSHMVSVDPEMAAE 901
 DB 715 LGKAIIVKRENSSONQWRFYQLTKLDSMHVEVNLTYCYQTFQTLDKTM-SIEFPEMLAE 773
 QY 902 IISVQVPKILSGVKPIYFH 921
 DB 774 IITNQIPKYSNGNIKKLLEH 793

Search completed: April 28, 2003, 13:52:28
 Job time : 33 secs